



# Blast 2 Sequences results

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Taxonomy

Structure

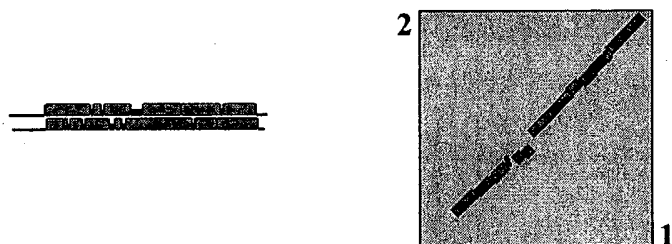
## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**  
 x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ Align

Sequence 1 gi 1362047 cysteine proteinase (EC 3.4.22.-) precursor - soybean Length 380 (1 .. 380)

Sequence 2 lcl|seq\_2

Length 366 (1 .. 366)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 204 bits (520), Expect = 4e-51  
 Identities = 133/336 (39%), Positives = 181/336 (53%), Gaps = 67/336 (19%)

```

Query: 59  ENYGRSYSTEEYLRRLGIFAQNMVRAAEHQALDPTAVHGVTFQSDLTEDEFKLYTGVN 118
          E++  ++ T+   R  IF  +  +  EH+A      H  T+FSDLT  +  +L
Sbjct: 56  EDHHLAFKTKFAKDHFRIFKHHFSQE-EHRAKS----HQKTRFSDLTGLKPLRLLD--- 107

Query: 119 GGFPSSNNAAGG--IAPPLEVDGLPE---NFDWREKGAVTEVKLQGRGSCWAFSTTGS 173
          PS+ +  G  +  P+   G  +  +FDW      QG CG CW+
Sbjct: 108 ---PSAPSEFRGQFLKAPIRDHGPSDAQTFDW-----QGSCGWCWS----- 146

Query: 174 EGANFLATGK-----LVSLSEQQLLDCKDNKCDITEKTSCDNGCN 212
          EGA+FL+TG      LVSLSEQQL+DCD++CD  E+  +CD+GCN
Sbjct: 147 EGAHFLSTGLPTS DLPVAVTGKFNFSVAVGALGLVSLSEQQLVDCDHECDPEERGACDSGCN 206

Query: 213 GGLMTNAYNYXXXXXXXXXXXXXYPYTGERGECKF-DPEKIAVKITNFTNIPADENQIAAY 271
          GGLMT A+ Y      YPYTG  + K   P KIA  + NF+  +   QIAA
Sbjct: 207 GGLMTTAFEYTLKAGGLMREEDYPYTGRFDKSKDRGPCKIAASVANFSVV-----QIAAN 261

Query: 272 LVKNGPLAMGVNAIFMQTYIGGVSCPLICKKRLNHGVL-----LVGYGAKGFSILRLGN 326
          LVKNGP A+ + ++  +  +G VSCP IC K  L+HGVL      LVGYG+  ++ +R
Sbjct: 262 LVKNGPNAVFMQSLDEELAVGIVSCPYICGK-HLDHGVLTYIGGLVGYGSGAYAPIRFKE 320

Query: 327 KPYWIIKNSWGEKWGEDGYKLCRGHGMCGINTMVS 362
          KPYWIIKNSWGE WGE+GYK+CRG  +CG+++MVS
Sbjct: 321 KPYWIIKNSWGESWGEEGYKICRGRNVCVDSMVS 356
  
```

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda K H  
 0.318 0.136 0.416

## Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1122

Number of Sequences: 0

Number of extensions: 96

Number of successful extensions: 4

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 380

length of database: 741,981,269

effective HSP length: 132

effective length of query: 248

effective length of database: 741,981,137

effective search space: 184011321976

effective search space used: 184011321976

T: 9

A: 40

X1: 16 ( 7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.7 bits)

S2: 77 (34.3 bits)